

Claims 1, 5, 7-9, 11, 13, 15, and 19 have been amended to more particularly point out and distinctly claim the subject matter that applicants regard as the invention. Specifically, claim 1, and all claims that depend therefrom, have been amended to recite an isolated nucleic acid molecule (i.e., instead of an isolated sequence) comprising a MEL7 promoter, to more accurately describe the statutory subject matter of the claim. Claim 1 has further been amended to recite that the MEL7 promoter comprises a sequence that is within 1560 nucleotides upstream of the MEL7 coding sequence (presented in SEQ ID NO:46) in cantaloupe melon genomic DNA. Support for this feature is found, *inter alia*, in the following sections: page 7 lines 6-7, where promoters of the invention are defined; page 11 lines 27-32, where it is described that the MEL7 promoter comprises regulatory regions found in melon genomic DNA upstream of the sequence corresponding to the MEL7 transcript, disclosed in GenBank accession Z70522 (and in the newly submitted SEQ ID NO:46); page 23 line 20 – page 25 line 16, in which it is clarified that the melon from which nucleic acids of the invention were isolated was cantaloupe; and page 25 lines 22-26 and Figure 3A-3C, which clarify that the MEL7 promoter fragment comprises 1.56 kb (i.e., 1560 nucleotides) upstream of the MEL5 coding sequence.

Claim 5 has been amended to specify that the MEL7 promoter sequence of SEQ ID NO:42 comprises the sequence from nucleotides 156-1708. Support for this feature is found in Figure 3A-3C, and on page 25 lines 22-26.

Claim 7 has been amended to depend from claim 1 instead of claim 5.

Claim 8 has been amended to recite that the MEL7 promoter (i.e., not the vector containing it) is operably linked to a heterologous nucleic acid coding sequence. Support for this feature is found, *inter alia*, on page 6 lines 35-42 and on page 12 lines 13-28.

Claim 9 has been amended to recite that the heterologous nucleic acid coding sequence (i.e., not the vector containing it) is operably linked to control sequences recognized by a host cell transformed with the vector. Support for this feature is found, *inter alia*, on page 4 lines 27-29, page 7 lines 6-10 and 32-39, page 12 lines 19-34, and on page 13 lines 16-21.

Claim 11 has been amended to depend from claim 7 instead of claim 9 or 10.

Claim 13 has been amended to specify that the claimed plant cell is transgenic, in order to more accurately describe the statutory subject matter of the claim. Claim 13 has further been amended to recite that the MEL7 promoter comprised by the transgenic plant cell is operably linked to a heterologous coding sequence. Support for this feature is found, *inter alia*, on page 6 line 39 – page 7 line 5, and on page 13, line 33-38.

Claim 15 has been amended to incorporate the steps previously recited in dependent claim 16. The preamble of claim 15 has been amended to reflect that the method encompassing all steps is a method for expressing a heterologous nucleic acid sequence in fruit of a transgenic fruit-bearing plant. Support for this feature is found, *inter alia*, on page 13 lines 13-26.

Claim 19 has been amended to recite that the heterologous nucleic acid, which was previously identified by the name "*sam-k*," encodes *S*-adenosylmethionine hydrolase (SAMase). Support for the feature that *sam-k* encodes SAMase is found, *inter alia*, on page 22 lines 3-5

Claim 20 has been added to more particularly point out and distinctly claim the subject matter that applicants regard as the invention. Claim 20 was previously encompassed in claim 11.

A marked-up copy of the amended claims is provided in Appendix A. A clean version of the entire set of pending claims is provided in Appendix B.

Amendment to the Specification

Please delete the paragraph on page 11, lines 28-35, and replace it with the following paragraph:

C¹⁰
RAP-screening was used to isolate a particularly abundant transcript fragment from ripe melon fruit. The isolated transcript (melrapF = MEL7, GenBank Accession Z70522; sequence provided in SEQ ID NO:46) was shown to be relatively fruit-specific and ripening-associated by Northern blot analysis. The transcript fragment was cloned and sequenced, and using gene-specific sequence information, upstream regulatory regions were amplified from melon genomic DNA. A second, related fruit-specific gene was identified from reports in the literature (MEL2, GenBank accession Z70521), and a corresponding upstream regulatory region was obtained using sequence information from the published cDNA clone. See Example 2.

Please delete Table 10 on page 36 and replace it with the following version of Table 10:

DESCRIPTION	SEQ ID NO
Adaptor (universal genome walker): 5'-GTAATACGACTCACTATAGGGCACGCGTGGTGGTCGACGGCCCGGCTGGT-3'	1
Adaptor, complimentary strand: 3'-H2N-CCCGACCA-PO4-5'	2
AP1 primer: 5'-GTA ATA CGA CTC ACT ATA GGG C-3'	3
AP2 primer: 5'-ACT ATA GGG CAC GCG TGG T-3'	4
PFAcol#1 primer: 5'-AAT TTG CTC CAA TAT CTT AGC TCT AC-3'	5
PFAcol#2 primer: 5'-AGA CAG CCA TTT CTT TTT GTA GAT AC-3'	6
NEB #1233 primer: 5'-AGC GGA TAA CAA TTT CAC ACA GGA-3'	7
ACO1ProR-a primer 5'-TAGACGGATCCTTCTTTTGTAGATACAAGAT-3'	8
E4UTR5'UP primer: 5'-GATCCATTATTAGAGATTGAGC-3'	9
E4UTR5'LO primer: 3'-CATGGCTCAATCTCTAATAATG-5'	10
cmDruP5'H3 primer: 5'-GGG CTG GAA AGC TTA AGA GAA ATT GGT A-3'	11
cmDruP3Bam primer: 5'-GGG GTT TTG TTT TTG GAT CCT GGG TGT GTT-3'	12
MAR AP1: 5'-CCATCCTAATACGACTCACTATAGGGC-3'	13
CSP: 5'-GGGCAGGTTTCTAGAATTCAGCGGCCGC-3'	14
pM7-5R-1' 5'-GTG AAA CTC GAC CCG TTC CTT AAA AAC TTC-3'	15
cmDruNcoSt 5'-GCTTTCCAATGAGAGCCATGGTTTTAAACCTT-3'	16
pMel2-outer: 5'-TAT TAC CTT CAC TGG ATC TCT TCC CTC-3'	17
pMel2-inner: 5'-GCCTTAAGCTTTGTTGATCATCCACATC-3'	18
MEL2_NcoR: 5'-GTT TGC ATT GTT TCC ATG GGA AA -3'	19
NEB 1233: 5'-AGC GGA TAA CAA TTT CAC ACA GGA-3'	20
H-T ₁₁ G: 5'-AAG CTT TTT TTT TTT G-3' (DD anchor primer, HindIII series)	21
H-T ₁₁ C: 5'-AAG CTT TTT TTT TTT C-3' (DD anchor primer, HindIII series)	22
H-T ₁₁ A: 5'-AAG CTT TTT TTT TTT A-3' (DD anchor primer, HindIII series)	23
H-AP1: 5'-AAG CTT GAT TGC C-3' (DD random primer, HindIII series)	24
H-AP2: 5'-AAG CTT CGA CTG T-3' (DD random primer, HindIII series)	25
H-AP3: 5'-AAG CTT TGG TCA G-3' (DD random primer, HindIII series)	26
H-AP4: 5'-AAG CTT CTC AAC G-3' (DD random primer, HindIII series)	27
H-AP5: 5'-AAG CTT AGT AGG C-3' (DD random primer, HindIII series)	28
H-AP6: 5'-AAG CTT GCA CCA T-3' (DD random primer, HindIII series)	29
H-AP7: 5'-AAG CTT AAC GAG G-3' (DD random primer, HindIII series)	30
H-AP8: 5'-AAG CTT TTA CCG C-3' (DD random primer, HindIII series)	31
6E-PF1: 5'-TTC TAG GCG AAA ACC AAG TGG GCC TAA T-3'	32
6E-PF2: 5'-CCC ACA CTG ACC CCA ACA AAC AAT AGC-3'	33
6EMELNcoP: 5'-AGGCCATGGTCGGTGCCGGGAAAA-3'	34
NEB #1233 (M13 Reverse, -40): 5'-AGC GGA TAA CAA TTT CAC ACA GGA-3'	35
2F-PF1: 5'-GA CAGTATAGTTCATGGCTTGGTTGG-3'	36
2F-PF2: 5'-AGGTTCTTTTAATCAGGCAATCTTCTT-3'	37
2FBamStart: 5'-GCGGGATCCTATTTTTGTGAATTGGAAATG-3'	38
NEB #1224 (M13 Forward, -40): 5'-CGCCAGGGTTTCCCAGTCACGAC-3'	39
1.35kb ACO1 promoter (-1256 to the translational start at +101, Figs. 1A-B)	40
ACO1/TE4 promoter (Figs. 2A-B)	41
MEL7 promoter (Figs. 3A-C)	42
MEL2 promoter (Figs. 4A-C)	43
melon 6E promoter (Figs. 6A-B)	44
melon 2F promoter (Figs. 7A-C)	45
MEL7 mRNA (GenBank Accession Z70522)	46

Please delete the paragraph on page 20, lines 38-41, and replace it with the following paragraph:

Sub D1
C12

A Basic BLASTN search (website at www.ncbi.nlm.nih.gov/BLAST/) of non-redundant nucleic acid sequence databases through NCBI (website at www.ncbi.nlm.nih.gov/index.html) indicated that the 1.3kb cmACO1 promoter sequence corresponds to a portion of the sequence found in GenBank at Accession Number X95551.

Please delete the paragraph on page 29, lines 29-33, and replace it with the following paragraph:

Sub D2
C13

A Basic BLASTN search (website at www.ncbi.nlm.nih.gov/BLAST/) of non-redundant nucleic acid sequence databases (consisting of all non-redundant GenBank+EMBL+DDBJ+PDB sequences, but no Expressed Sequencing Tags (ESTs), STS, Genome Survey Sequence, or High Throughput Genomic Sequences) through NCBI (website at www.ncbi.nlm.nih.gov/index.html) revealed no significant database matches to the sequence of either the 6E or 2F promoters.

Remarks

The replacement paragraph on page 11 lines 28-35, and the replacement Table 10 on page 36 differ from the respective deleted paragraph and table in that they include a sequence listing for MEL7mRNA sequence (SEQ ID NO:46), which is added with the replacement Sequence Listing filed herewith.

The replacement paragraphs on page 20 lines 38-41, and on page 29 lines 29-33, differ from the respective deleted paragraphs in that hyperlinks (including text that may be formatted as active links) have been deleted and replaced with descriptions of websites.

A marked-up version of the replacement paragraphs and table is provided as Appendix C. No new matter is introduced by the amendments to the specification.

REPLY

Objections to the Specification

Regarding the Examiner's objection to the specification based on the improper inclusion of hyperlinks, hyperlinks and text that may be formatted as an active link have been removed. However, the instant amendments do not remove the citation of internet addresses. Applicants respectfully maintain that the USPTO policy, as set forth in M.P.E.P. 608.01 and 608.01(p) does not specifically disallow citation of internet

addresses. Rather, the policy disallows hyperlinks and other forms of browser executable code, as well as incorporation by reference of hyperlinks and other forms of browser-executable code. Neither is included in the specification as amended.

Objections to the Claims

Regarding the Examiner's objection to the claims based on informalities in claims 13 and 15, the instant amendments to the claims correct these informalities.

Claim Rejections – 35 USC § 112, 2nd paragraph

The Examiner has rejected claims 1-3, 5, and 7-19, under 35 USC § 112, second paragraph, for failing to particularly point out and distinctly claim the subject matter which applicants regard as the invention.

Applicants have cancelled claims 2, 3, and 16-18.

With regard to the term "characterized by" in claim 1, the amended claim no longer recites this term.

With regard to the recitation of the term "MEL7" of claim 1, the Examiner has maintained that recitation of MEL7 renders the claim indefinite since the name "MEL7" is arbitrarily assigned and does not clearly identify the promoter. Applicants have amended the claim to specify that the MEL7 gene comprises the coding sequence provided in SEQ ID NO:46 (GenBank accession Z70522), and that the MEL7 promoter comprises sequences that naturally occur upstream of this coding sequence in melon genomic DNA. The amended claim further specifies the essential trait of the claimed promoter in reciting that the MEL7 promoter promotes fruit-associated expression of a transgene to which it is operably linked.

With regard to the term "operably linked to a heterologous nucleic acid coding sequence" in claim 8, this claim has been amended to specify that the MEL7 promoter is operably linked to the heterologous nucleic acid coding sequence.

With regard to the term "operably linked to control sequences" in claim 9, this claim has been amended to specify that the heterologous coding sequence is operably linked to the control sequences.

With regard to the recitation of "sam-k" in claim 19, this claim has been amended to specify that the heterologous nucleic acid coding sequence encodes S-adenosylmethionine hydrolase.

Claim Rejections – 35 USC § 112, 1st paragraph

The Examiner has further rejected claims 1-3 and 13-19 under 35 USC § 112, first paragraph, for containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the art that the inventors had possession of the claimed invention.

The Examiner has alleged that the claims are "broadly drawn towards any isolated nucleic acid sequence comprising any fruit-associated promoter of any MEL7 gene of any melon," wherein the promoter has certain named characteristics. Applicants respectfully disagree and submit that one of ordinary skill in the art reading the specification would understand the meaning of the MEL7 promoter. Applicants have indicated on page 11 line 29 and on page 24 lines 33-38 that MEL7 refers to the gene having the transcript whose sequence is disclosed in GenBank accession Z70522. Thus the claims are not directed to "any promoter of any MEL7 gene." The amendment to claim 1 that incorporates sequence information for the MEL7 gene specifies that the invention is directed to a promoter from a single MEL7 gene.

The Examiner has further rejected claims 1-3 and 13-19 for lack of enablement and has maintained that the specification, while being enabling for the MEL7 promoter set forth in SEQ ID NO:42, does not reasonably provide enablement for other nucleic acid sequence comprising other promoters of other MEL7 genes. To the extent that the Examiner's rejections are based on the belief that the claims encompass promoters from multiple MEL7 genes, the amendment to claim 1 that incorporates the sequence information for the MEL7 gene overcomes this rejection. However, if the Examiner is further implying that the only promoter sequence enabled is that provided in SEQ ID NO:42, applicants respectfully disagree. It is well known in the art that it is possible to alter the sequence of an isolated promoter, for instance by small insertions or deletions, and/or by 5' truncations, and to empirically test the activity of the altered promoter for its ability to direct gene expression in the same manner of the originally isolated promoter. The specification teaches methods for testing the activity of a fruit-associated promoter sequences by generating chimeric constructs in which the promoter is operably linked to GUS coding sequences and testing the activity of the construct in transformed fruit tissue (Example 2, page 25 line 18 – page 26 line 21; Example 4, page 31 line 5 – page 33 line 20). It is further well known that polymorphisms that do not affect the promoter activity may naturally occur. Promoters having such minor alterations with respect to the exemplified MEL7 sequence are encompassed by amended claim 1, which recites a promoter whose sequence is within 1560 nucleotides upstream of the MEL7 coding sequence (exemplified by the upstream sequence presented as SEQ ID NO:42), which is

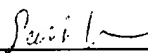
capable of directing fruit-associated gene expression of a heterologous coding sequence to which it is operably linked.

CONCLUSION

In view of the claim amendments and for the above reasons, it is believed that all of the rejections are overcome, and that the claims are in condition for allowance.

Respectfully submitted,

Dated: August 5, 2002



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APPENDIX A

1. (Twice amended) An isolated nucleic acid molecule [sequence] comprising a [melon fruit-associated promoter] MEL7 promoter, wherein the MEL7 promoter comprises a sequence that is within 1560 nucleotides upstream of the MEL7 coding sequence, as presented in SEQ ID NO:46, in cantaloupe melon genomic DNA, and wherein the MEL7 promoter, when operably linked to a transgene, promotes [characterized by the ability to promote] fruit-associated expression of the [a] transgene [to which said melon fruit-associated promoter sequence is operably linked].

5. (Twice amended) The isolated nucleic acid molecule [sequence] of claim 1, wherein the [melon fruit-associated promoter] MEL7 promoter has the nucleotide sequence presented as nucleotides 156-1708 of SEQ ID NO:42.

7. (Twice amended) A plant expression vector comprising the MEL7 promoter of claim 1 [5].

8. (Amended) The plant expression vector of claim 7, wherein the MEL7 promoter is operably linked to a heterologous nucleic acid coding sequence.

9. (Amended) The plant expression vector of Claim 8, wherein the heterologous nucleic acid coding sequence is operably linked to control sequences recognized by a host cell transformed with the vector.

11. (Amended) A plant cell comprising the plant expression vector of claim 7 [9 or 10].

13. (Amended) A transgenic plant cell comprising the isolated nucleic acid molecule [a melon fruit-associated promoter] according to claim 1, wherein the MEL7 promoter is operably linked to a heterologous nucleic acid coding sequence.

15. (Amended) A method of expressing a heterologous nucleic acid sequence in fruit of a transgenic plant [a plant cell], comprising:

(a) transforming [a] plant cells [cell] with a nucleic acid construct comprising a MEL7 [melon] promoter according to claim 1, wherein the MEL7 promoter is operably linked to a heterologous nucleic acid coding sequence;

(b) culturing said plant cells in a culturing medium containing a selection agent to select for transformed plant cells; and

(c) growing said transformed plant cells to produce a transgenic fruit-bearing plant, wherein the heterologous nucleic acid sequence is expressed in fruit of said transgenic fruit-bearing plant.

19. (Amended) The method according to claim 18, wherein said heterologous nucleic acid coding sequence encodes S-adenosylmethionine hydrolase (SAMase) [is sam-k] and wherein [the mature fruit of] said transgenic fruit-bearing plant produces

mature fruit that exhibit [exhibits] a decrease in ethylene production relative to a non-transgenic plant.

APPENDIX B

1. An isolated nucleic acid molecule comprising a MEL7 promoter, wherein the MEL7 promoter comprises a sequence that is within 1560 nucleotides upstream of the MEL7 coding sequence, as presented in SEQ ID NO:46, in cantaloupe melon genomic DNA, and wherein the MEL7 promoter, when operably linked to a transgene, promotes fruit-associated expression of the transgene.

5. The isolated nucleic acid molecule of claim 1, wherein the MEL7 promoter has the nucleotide sequence presented as nucleotides 156-1708 of SEQ ID NO:42.

7. A plant expression vector comprising the MEL7 promoter of claim 1.

8. The plant expression vector of claim 7, wherein the MEL7 promoter is operably linked to a heterologous nucleic acid coding sequence.

9. The plant expression vector of Claim 8, wherein the heterologous nucleic acid coding sequence is operably linked to control sequences recognized by a host cell transformed with the vector.

10. The plant expression vector of claim 9, wherein said heterologous nucleic acid coding sequence encodes *S*-adenosylmethionine hydrolase (SAMase).

11. A plant cell comprising the plant expression vector of claim 7.

12. A mature plant comprising the plant cell of claim 11.

13. A transgenic plant cell comprising the isolated nucleic acid molecule according to claim 1, wherein the MEL7 promoter is operably linked to a heterologous nucleic acid coding sequence.

14. A mature plant comprising the plant cell of claim 13.

15. A method of expressing a heterologous nucleic acid sequence in fruit of a transgenic plant, comprising:

- (a) transforming plant cells with a nucleic acid construct comprising a MEL7 promoter according to claim 1, wherein the MEL7 promoter is operably linked to a heterologous nucleic acid coding sequence;
- (b) culturing said plant cells in a culturing medium containing a selection agent to select for transformed plant cells; and
- (c) growing said transformed plant cells to produce a transgenic fruit-bearing plant,

wherein the heterologous nucleic acid sequence is expressed in fruit of said transgenic fruit-bearing plant.

19. The method according to claim 18, wherein said heterologous nucleic acid coding sequence encodes *S*-adenosylmethionine hydrolase (SAMase) and wherein said transgenic fruit-bearing plant produces mature fruit that exhibit a decrease in ethylene production relative to a non-transgenic plant.

20. A plant cell comprising the plant expression vector of claim 10.

APPENDIX C

Page 11, lines 28-35

RAP-screening was used to isolate a particularly abundant transcript fragment from ripe melon fruit. The isolated transcript (melrapF = MEL7, GenBank Accession Z70522; sequence provided in SEQ ID NO:46) was shown to be relatively fruit-specific and ripening-associated by Northern blot analysis. The transcript fragment was cloned and sequenced, and using gene-specific sequence information, upstream regulatory regions were amplified from melon genomic DNA. A second, related fruit-specific gene was identified from reports in the literature (MEL2, GenBank accession Z70521), and a corresponding upstream regulatory region was obtained using sequence information from the published cDNA clone. See Example 2.

Page 20, lines 38-41

A Basic BLASTN search (website at www.ncbi.nlm.nih.gov/BLAST/) [[\(http://www.ncbi.nlm.nih.gov/BLAST/\)](http://www.ncbi.nlm.nih.gov/BLAST/)] of non-redundant nucleic acid sequence databases through NCBI (website at www.ncbi.nlm.nih.gov/index.html) [[\(http://www.ncbi.nlm.nih.gov/index.html\)](http://www.ncbi.nlm.nih.gov/index.html)] indicated that the 1.3kb cmACO1 promoter sequence corresponds to a portion of the sequence found in GenBank at Accession Number X95551.

Page 29, lines 29-33

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Page 36, Table 10

DESCRIPTION	SEQ ID NO
Adaptor (universal genome walker): 5'-GTAATACGACTCACTATAGGGCACGCGTGGTGGTCGACGGCCCGGGCTGGT-3'	1
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AP1 primer: 5'-GTA ATA CGA CTC ACT ATA GGG C-3'	3
AP2 primer: 5'-ACT ATA GGG CAC GCG TGG T-3'	4
PFACol#1 primer: 5'-AAT TTG CTC CAA TAT CTT AGC TCT AC-3'	5
PFACol#2 primer: 5'-AGA CAG CCA TTT CTT TTT GTA GAT AC-3'	6
NEB #1233 primer: 5'-AGC GGA TAA CAA TTT CAC ACA GGA-3'	7
ACO1ProR-a primer 5'-TAGACGGATCCTTCTTTTGTAGATACAAGAT-3'	8
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E4UTR5'LO primer: 3'-CATGGCTCAATCTCTAATAATG-5'	10
cmDruP5'H3 primer: 5'-GGG CTG GAA AGC TTA AGA GAA ATT GGT A-3'	11
cmDruP3Bam primer: 5'-GGG GTT TTG TTT TTG GAT CCT GGG TGT GTT-3'	12
MAR AP1: 5'-CCATCCTAATACGACTCACTATAGGGC-3'	13
CSP: 5'-GGGCAGGTTTCTAGAATTCAGCGGCCGC-3'	14
pM7-5R-1' 5'-GTG AAA CTC GAC CCG TTC CTT AAA AAC TTC-3'	15
cmDruNcoSt 5'-GCTTTCCAATGAGAGCCATGGTTTTAAACCTT-3'	16
pMel2-outer: 5'-TAT TAC CTT CAC TGG ATC TCT TCC CTC-3'	17
pMel2-inner: 5'-GCCTTAAGCTTTGTTGATCATCCACATC-3'	18
MEL2_NcoR: 5'-GTT TGC ATT GTT TCC ATG GGA AA -3'	19
NEB 1233: 5'-AGC GGA TAA CAA TTT CAC ACA GGA-3'	20
H-T ₁₁ G: 5'-AAG CTT TTT TTT TTT G-3' (DD anchor primer, HindIII series)	21
H-T ₁₁ C: 5'-AAG CTT TTT TTT TTT C-3' (DD anchor primer, HindIII series)	22
H-T ₁₁ A: 5'-AAG CTT TTT TTT TTT A-3' (DD anchor primer, HindIII series)	23
H-AP1: 5'-AAG CTT GAT TGC C-3' (DD random primer, HindIII series)	24
H-AP2: 5'-AAG CTT CGA CTG T-3' (DD random primer, HindIII series)	25
H-AP3: 5'-AAG CTT TGG TCA G-3' (DD random primer, HindIII series)	26
H-AP4: 5'-AAG CTT CTC AAC G-3' (DD random primer, HindIII series)	27
H-AP5: 5'-AAG CTT AGT AGG C-3' (DD random primer, HindIII series)	28
H-AP6: 5'-AAG CTT GCA CCA T-3' (DD random primer, HindIII series)	29
H-AP7: 5'-AAG CTT AAC GAG G-3' (DD random primer, HindIII series)	30
H-AP8: 5'-AAG CTT TTA CCG C-3' (DD random primer, HindIII series)	31
6E-PF1: 5'-TTC TAG GCG AAA ACC AAG TGG GCC TAA T-3'	32
6E-PF2: 5'-CCC ACA CTG ACC CCA ACA AAC AAT AGC-3'	33
6EMELNcoP: 5'-AGGCCATGGTCGGTGCCGGGAAAA-3'	34
NEB #1233 (M13 Reverse, -40): 5'-AGC GGA TAA CAA TTT CAC ACA GGA-3'	35
2F-PF1: 5'-GA CAGTATAGTTCATGGCTTGTTGG-3'	36
2F-PF2: 5'-AGGTTCTTTTAATCAGGCAATCTTCTT-3'	37
2FBamStart: 5'-GCGGGATCCTATTTTTGTGAATTGGAAATG-3'	38
NEB #1224 (M13 Forward, -40): 5'-CGCCAGGGTTTCCAGTCACGAC-3'	39
1.35kb ACO1 promoter (-1256 to the translational start at +101, Figs. 1A-B)	40
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MEL7 mRNA (GenBank Accession Z70522)	46